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YEAST TOPOISOMERASE II  E. COLI GYRASE B  E. COLI GYRASE A
HUMAN SUCCINYL CoA-TRANSFERASE  E. COLI ACETATE Co-A TRASNFERASE β  E. COLI ACETATE Co-A TRASNFERASE β
B. SUBTILIS DNA POL III α  E. COLI DNA POL III ε  E. COLI DNA POL III ε
YEAST HISTIDINE BIOSYNTHESIS HIS2 E. COLI HISTIDINE BIOSYNTHESIS HIS10
HUMAN $\delta$ -1-PYRROLINE-5-CARBOXYLATE SYNTHETASE $\neg$

FIG. 1A

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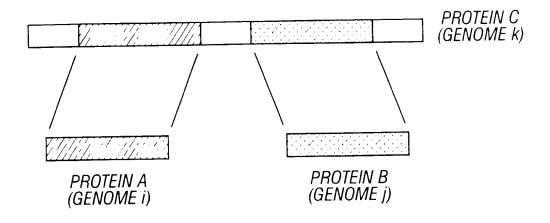


FIG. 1B

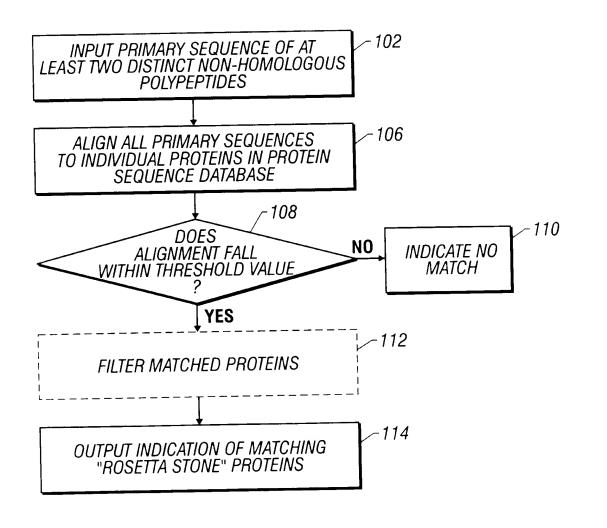


FIG. 2A



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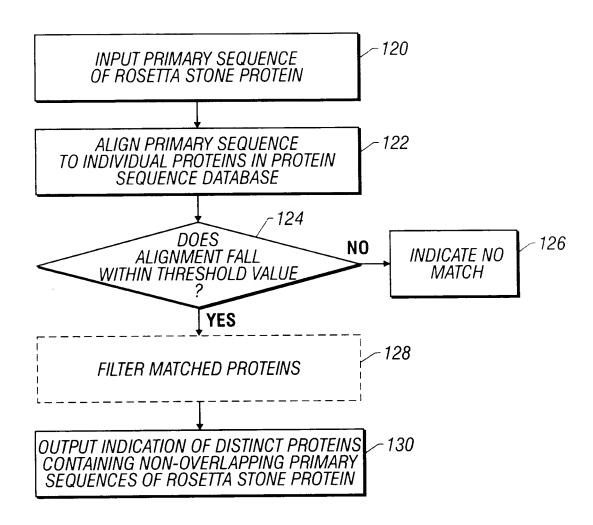
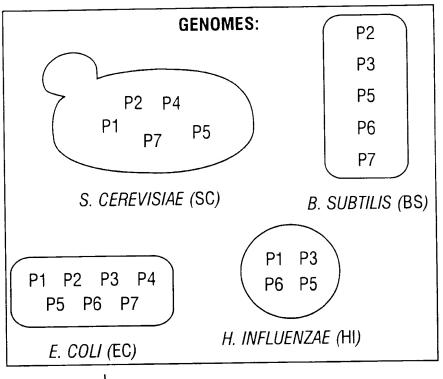
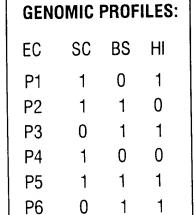


FIG. 2B

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1

**P7** 

0

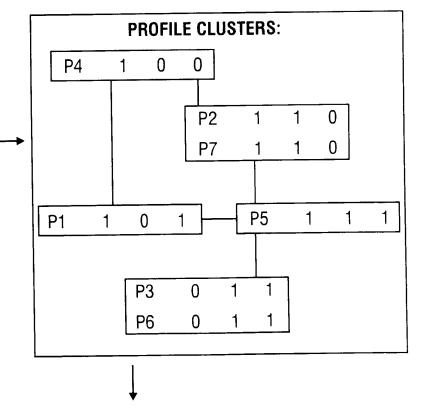


FIG. 3

**CONCLUSION:** P2 AND P7 ARE FUNCTIONALLY LINKED, P3 AND P6 ARE FUNCTIONALLY LINKED

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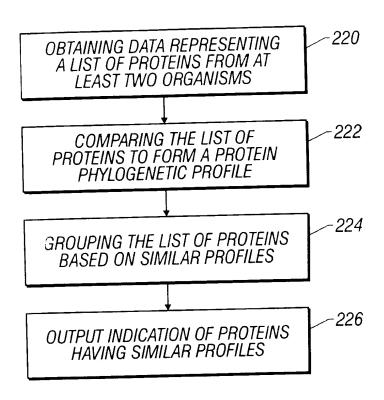


FIG. 4A

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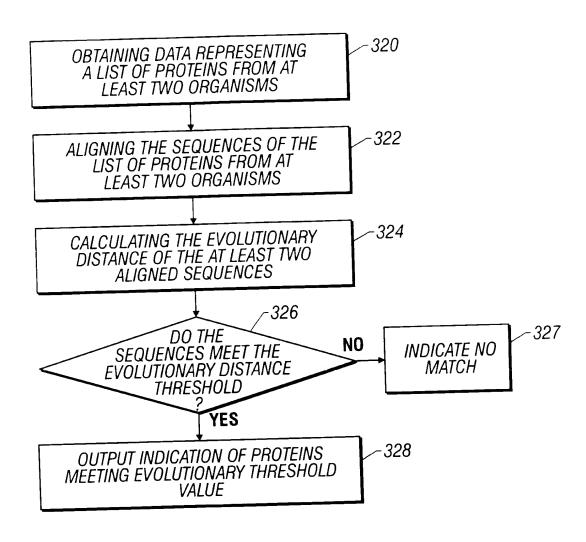


FIG. 4B

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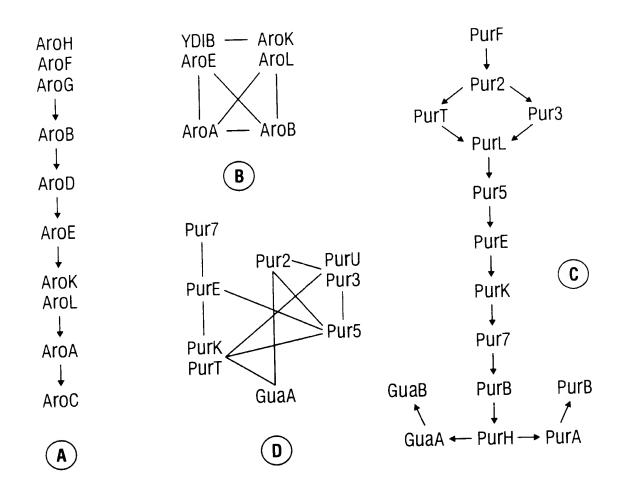
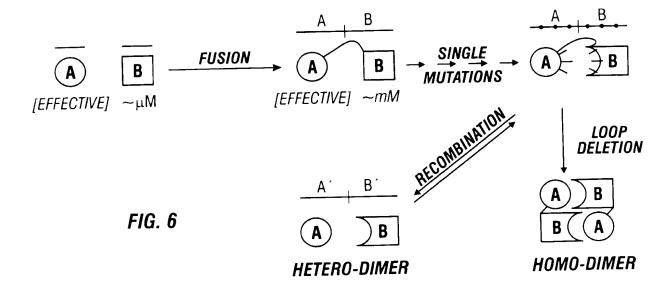


FIG. 5





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ROMBINED COMPUTATIONAL METHODS FOR DETECTING PROTEIN FUNCTION AND PROTEIN-PROTEIN INTERACTIONS FROM GENOME SEQUENCES

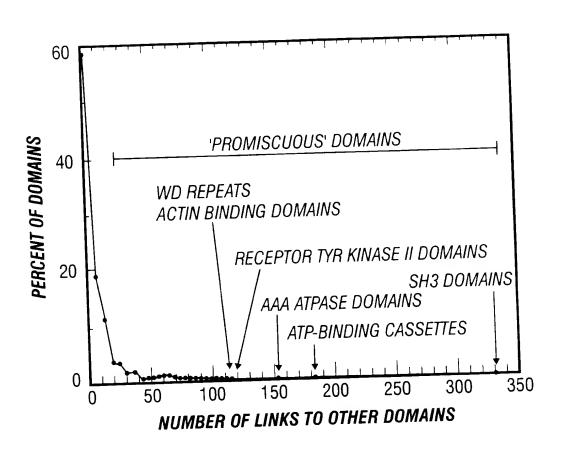


FIG. 7



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## INITIAL PROFILE

#### ONE BIT DIFFERENT

1877 PgsA PHOSPHOLIPID SYNTHESIS 2895 YGGH HYPOTHETICAL

0648 YBEX HYPOTHETICAL

3624 RL34 RIBOSOME L34

3222 RL36 *RIBOSOME L36* 

3115 RL27 RIBOSOME L27

3097 RS15 RIBOSOME S15

2731 YQCB HYPOTHETICAL

0058 YABO HYPOTHETICAL

1059 YCEC HYPOTHETICAL

0229 RFH PEPTIDE RELEASE FACTOR

2539 ClpB HEAT SHOCK PROTEIN

4071 YJFH HYPOTHETICAL

3230 RS14 RIBOSOME S14

1387 G3P3 DEHYDROGENASE

3242 RL4 RIBOSOME L4 1945 NONE *HYPOTHETICAL* 

2561 GrpE CO-CHAPERONE

3661 GidB GLUCOSE INHIB. DIVISION

3232 RL24 RIBOSOME L24

3210 DEF POLYPEPTIDE DEFORMYLASE

1684 RL20 RIBOSOME L20

0188 MesJ CELL CYCLE PROTEIN

2553 RF19 *RIBOSOME L19* 

3116 RL21 RIBOSOME L21

4094 RL9 *RIBOSOME L9* 

2567 SmpB SMALL PROTEIN B

3217 RL17 RIBOSOME L17 1177 PTH PEPTIDYL-tRNA HYDROLASE 2518 RNC RIBONUCLEASE III

3885 RL7 RIBOSOME L7

3224 RL15 RIBOSOME L15

FIG. 8A



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### INITIAL PROFILE

### ONE BIT DIFFERENT

3132 RP54 SIGMA FACTOR

1174 DHAR OPERON REGULATION
3345 RtcR TRANSCRIPTION REGULATOR
BINDS SIGMA FACTOR RP54
0205 MItD LYTIC MUREINE
TRANSGLYCOSYLASE

0624 Roda *ROD SHAPED DET.* 0089 FtsW *CELL DIVISION* 1163 AIr2 *ALANINE RACEMASE* 1070 YCEG *HYPOTHETICAL* 

4060 AmiB *Nam-Ala AMIDASE* 3948 AIr1 *ALANINE RACEMASE* 2890 YGGW *HYPOTHETICAL* 

1889 FliD FLAG. HOOK

1910 FliM *MOTOR* 1046 FlgB *FLAG BASAL* 

1915 Flir FLAG BIOSYNTH
1914 FliQ FLAG BIOSYNTH
1911 Flin MOTOR
1858 Mota MOTILITY
1056 FlgL FLAG HOOK
1051 FlgG FLAG HOOK/BASAL
1050 FlgF FLAG HOOK/BASAL
1049 FlgE FLAG HOOK/BASAL
1047 FlgC FLAG BASAL BODY
1055 FlgK FLAG HOOK

FIG. 8B



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COMBINED COMPUTATIONAL METHODS FOR ETECTING PROTEIN FUNCTION AND PROTEIN-PROTEIN INTERACTIONS FROM GENOME SEQUENCES

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# INITIAL PROFILE

#### ONE BIT DIFFERENT

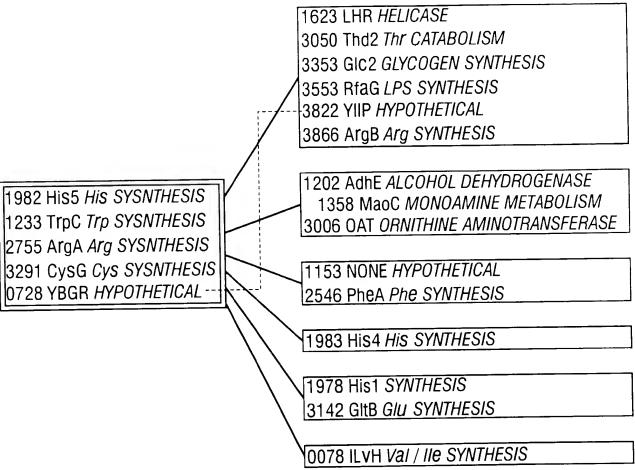


FIG. 8C

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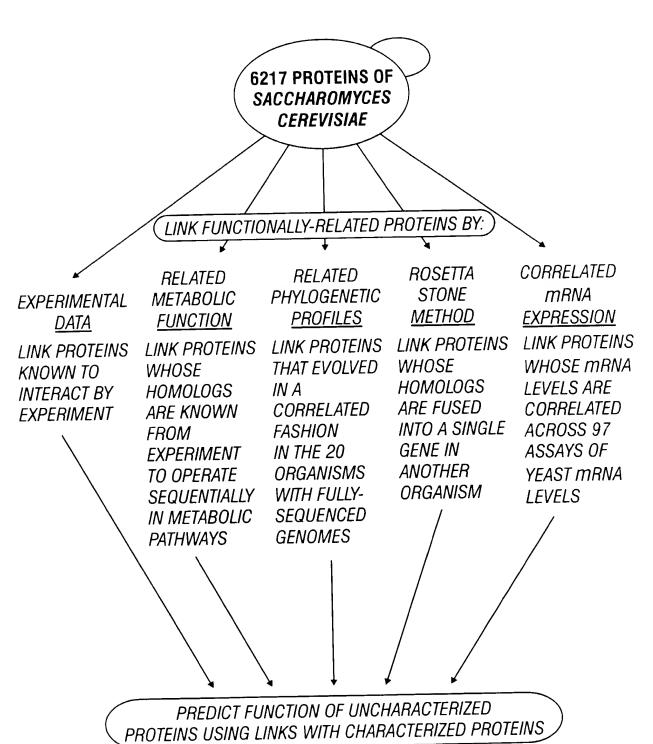


FIG. 9

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YCR083W HOMOLOGY TO THIOREDOXIN

**MRPL2** 

CONSERVED PROTEIN

FAMILY OF

YGR021W —— MEMBER OF HIGHLY UNKNOWN FUNCTION

MITOCHONDRIA PREDICTED TO TARGET YGL236C HOMOLOGY TO CONSERVED gidA FAMILY, UNKNOWN FUNCTION YOLOGOC HOMOLOGY TO HYPOTHETICAL C. ELEGANS PROTEIN MO2F4.4 SYNTHESIS **PROTEIN** YDR116C HOMOLOGY TO BACTERIAL RIBOSOMAL L1 PROTEIN YDL036C HOMOLGY TO RIB2 / PSEUDOURIDINE SYNTHASB YHR189W HOMOLOGY TO PEPTIDYL-TRNA HYDROLASE SIS1/XDJ1 HOMOLGY TO DNAJ HEAT SHOCK PROTEIN YJR113C HOMOLOGY TO RIBOSOMAL PROTEIN S7 YGL068W PROBABLE RIBOSOMAL PROTEIN L12 PDR13/SSE1/LHS1 HOMOLOGY TO HSp70 MGE1 HEAT SHOCK PROTEIN/CHAPERONE MRF1 PEPTIDE CHAIN RELEASE FACTOR TPI1 TRIOSE PHOSPHATE ISOMERASE MSY1 TYROSYL-TRNA SYNTHETASE ADE3 C1-THF SYNTHASE, MIS1 C1-THF SYNTHASE RIB2 DRAP DEAMINASE RIBOSOMAL **PROTEINS** KNOWN MRPS28 MRPL23 MRPL10 MRPL16 MRPL6 **MRPS9 MRPL7** 

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FIG. 10

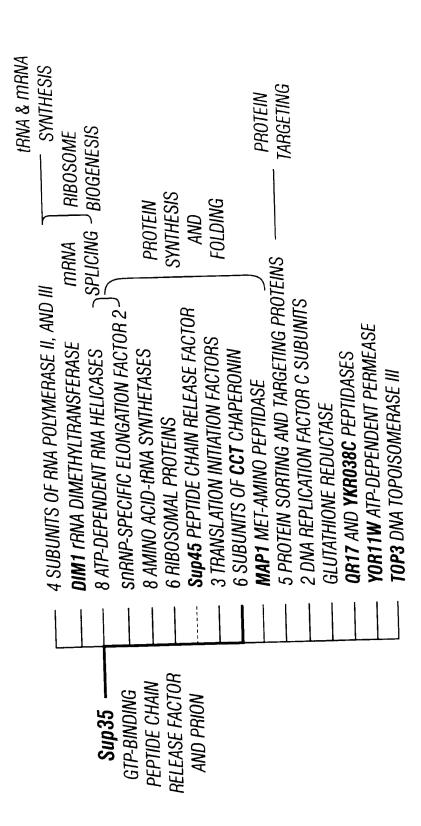


FIG. 11A

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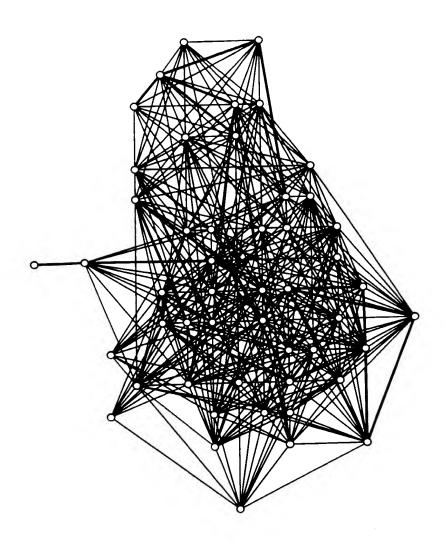


FIG. 11B

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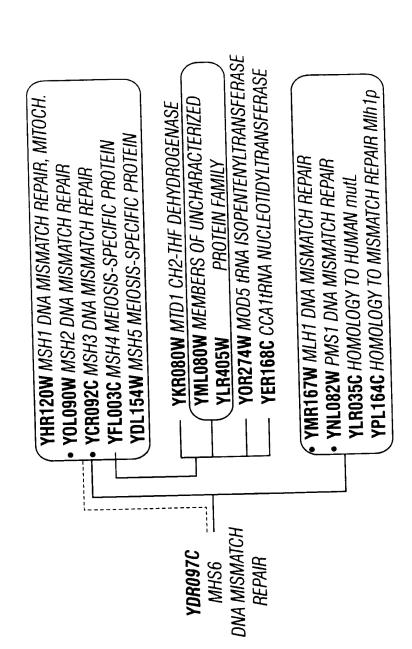


FIG. 12